

SEQUENCE LISTING

<110> Andersen, Carsten
Borchert, Torben Vedel
Nielsen, Bjarne Ronfeldt

<120> Variants with altered properties

<130> 10004.204-US

<160> 20

<170> PatentIn version 3.1

<210> 1

<211> 1455

<212> DNA

<213> Bacillus sp.

<220>

<221> CDS

<222> (1)..(1455)

<223> SP690

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Thr	Arg	Asn	Gln	Leu	Gln	Ala	Ala	Val	Thr	Ser	Leu	Lys	Asn	Asn	Gly	
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att	cag	gta	tat	ggt	gat	gtc	gtc	atg	aat	cat	aaa	ggt	gga	gca	gat	336
Ile	Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp	
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Gly	Thr	Glu	Ile	Val	Asn	Ala	Val	Glu	Val	Asn	Arg	Ser	Asn	Arg	Asn	
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Gln	Glu	Thr	Ser	Gly	Glu	Tyr	Ala	Ile	Glu	Ala	Trp	Thr	Lys	Phe	Asp	
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Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp	
180 185 190	
aca gag aat ggc aac tat gac tat ctt atg tat gca gac gtg gat atg	624
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met	
195 200 205	
gat cac cca gaa gta ata cat gaa ctt aga aac tgg gga gtg tgg tat	672
Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr	
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Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr	
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Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr	
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Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser	
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<212> PRT

<213> Bacillus sp.

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Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
 35 40 45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
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Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
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Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp

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His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys 165 170 175		
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp 180 185 190		
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met 195 200 205		
Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr 210 215 220		
Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His 225 230 235 240		
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr 245 250 255		
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Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys 305 310 315 320		
His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro 325 330 335		
Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala 340 345 350		

Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
370 375 380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
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Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
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Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
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Val Trp Val Lys Gln
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<223> SP722

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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
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Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
35 40 45

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Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr	
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gat tta ggg gaa ttt aat caa aag ggg acg gtt cgt act aag tat ggg	240
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly	
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Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly	
85 90 95	
gtt caa gtt tat ggg gat gta gtg atg aac cat aaa gga gga gct gat	336
Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp	
100 105 110	
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Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn	
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Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr	
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His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg	
165 170 175	
atc tac aaa ttc cga ggt gat ggt aag gca tgg gat tgg gaa gta gat	576
Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp	
180 185 190	
tcg gaa aat gga aat tat gat tat tta atg tat gca gat gta gat atg	624
Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met	
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gat cat ccg gag gta gta aat gag ctt aga aga tgg gga gaa tgg tat	672
Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr	
210 215 220	
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Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val	
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 <213> Bacillus sp.

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Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp	35	40	45
Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr	50	55	60
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly	65	70	75
Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly	85	90	95
Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp	100	105	110
Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn	115	120	125
Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp	130	135	140
Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr	145	150	155
His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg	165	170	175
Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp	180	185	190
Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met	195	200	205
Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr	210	215	220
Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His	225	230	235
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala	245	250	255

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260 265 270

Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300

Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
385 390 395 400

Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
435 440 445

Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
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 Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
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 Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
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 65 70 75 80
 aaa gct caa tat ctt caa gcc att caa gcc gcc cac gcc gct gga atg 288
 Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
 85 90 95
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 Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
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 Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
 130 135 140
 ccc ggg cgg ggc aac acc tac tcc agc ttt aag tgg cgc tgg tac cat 480
 Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
 145 150 155 160
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 Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
 165 170 175
 aaa ttc cgc ggc atc ggc aaa gcg tgg gat tgg gaa gta gac acg gaa 576
 Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
 180 185 190

aac gga aac tat gac tac tta atg tat gcc gac ctt gat atg gat cat	624
Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His	
195 200 205	
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Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn	
210 215 220	
aca acg aac att gat ggg ttc cgg ctt gat gcc gtc aag cat att aag	720
Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys	
225 230 235 240	
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Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly	
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aag ccg cta ttt acc gtc ggg gaa tat tgg agc tat gac atc aac aag	816
Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys	
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ttg cac aat tac att acg aaa aca gac gga acg atg tct ttg ttt gat	864
Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp	
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gcc ccg tta cac aac aaa ttt tat acc gct tcc aaa tca ggg ggc gca	912
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Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln	
325 330 335	
gcg ctg cag tca tgg gtc gac cca tgg ttc aaa ccg ttg gct tac gcc	1056
Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala	
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Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp	
355 360 365	
tat tat ggc att cca caa tat aac att cct tcg ctg aaa agc aaa atc	1152
Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile	
370 375 380	
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465					470				475						480		
gtt	cct	aga	aaa	acg	acc	gtt	tct	acc	atc	gct	cgg	ccg	atc	aca	acc	1488	
Val	Pro	Arg	Lys	Thr	Thr	Val	Ser	Thr	Ile	Ala	Arg	Pro	Ile	Thr	Thr		
				485					490					495			
cga	ccg	tgg	act	ggg	gaa	ttc	gtc	cgt	tgg	acc	gaa	cca	cgg	ttg	gtg	1536	
Arg	Pro	Trp	Thr	Gly	Glu	Phe	Val	Arg	Trp	Thr	Glu	Pro	Arg	Leu	Val		
			500					505					510				
gca	tgg	cct	tga													1548	
Ala	Trp	Pro															
		515															

<210> 6
 <211> 515
 <212> PRT
 <213> Bacillus stearothermophilus

<400> 6

Ala	Ala	Pro	Phe	Asn	Gly	Thr	Met	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Leu		
1				5					10					15			
Pro	Asp	Asp	Gly	Thr	Leu	Trp	Thr	Lys	Val	Ala	Asn	Glu	Ala	Asn	Asn		
			20					25					30				
Leu	Ser	Ser	Leu	Gly	Ile	Thr	Ala	Leu	Trp	Leu	Pro	Pro	Ala	Tyr	Lys		
			35				40					45					
Gly	Thr	Ser	Arg	Ser	Asp	Val	Gly	Tyr	Gly	Val	Tyr	Asp	Leu	Tyr	Asp		
	50					55					60						
Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr		
65					70					75					80		
Lys	Ala	Gln	Tyr	Leu	Gln	Ala	Ile	Gln	Ala	Ala	His	Ala	Ala	Gly	Met		
				85				90						95			
Gln	Val	Tyr	Ala	Asp	Val	Val	Phe	Asp	His	Lys	Gly	Gly	Ala	Asp	Gly		
			100					105					110				
Thr	Glu	Trp	Val	Asp	Ala	Val	Glu	Val	Asn	Pro	Ser	Asp	Arg	Asn	Gln		
		115					120					125					

Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
130 135 140

Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
145 150 155 160

Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
165 170 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
180 185 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
195 200 205

Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn
210 215 220

Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
225 230 235 240

Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly
245 250 255

Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
260 265 270

Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp
275 280 285

Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala
290 295 300

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
305 310 315 320

Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
325 330 335

Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
340 345 350

Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
355 360 365

Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
370 375 380

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
385 390 395 400

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly
405 410 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
435 440 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
450 455 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
465 470 475 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr
485 490 495

Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
500 505 510

Ala Trp Pro
515

<210> 7
<211> 1920
<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (421)..(1872)
<223> Termamyl

<400> 7
cggaagattg gaagtacaaa aataagcaaa agattgtcaa tcatgtcatg agccatgcgg 60
gagacggaaa aatcgtotta atgcacgata tttatgcaac gttcgcagat gctgctgaag 120
agattattaa aaagctgaaa gcaaaaggct atcaattggt aactgtatct cagcttgaag 180
aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatata ggcgcttttc 240

ttttggaaga aaatataggg aaaatggtac ttgttaaaaa ttcggaatat ttatacaaca	300
tcatatgttt cacattgaaa ggggaggaga atcatgaaac aacaaaaacg gctttacgcc	360
cgattgctga cgctgttatt tgcgctcatt ttcttgctgc ctcatctctgc agcagcggcg	420
gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro 1 5 10 15	468
aat gac ggc caa cat tgg agg cgt ttg caa aac gac tcg gca tat ttg Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu 20 25 30	516
gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly 35 40 45	564
acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu 50 55 60	612
ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys 65 70 75 80	660
gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn 85 90 95	708
gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr 100 105 110	756
gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val 115 120 125	804
att tca gga gaa cac cta att aaa gcc tgg aca cat ttt cat ttt ccg Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro 130 135 140	852
ggg cgc ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe 145 150 155 160	900
gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys 165 170 175	948
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn 180 185 190	996
tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val 195 200 205	1044
gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln 210 215 220	1092

ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt	1140
Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe	
225 230 235 240	
ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg	1188
Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met	
245 250 255	
ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac	1236
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn	
260 265 270	
tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt	1284
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu	
275 280 285	
cat tat cag ttc cat gct gca tgc aca cag gga ggc ggc tat gat atg	1332
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met	
290 295 300	
agg aaa ttg ctg aac ggt acg gtc gtt tcc aag cat ccg ttg aaa tgc	1380
Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser	
305 310 315 320	
gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tgc ctt gag	1428
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu	
325 330 335	
tgc act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc	1476
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu	
340 345 350	
aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg	1524
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly	
355 360 365	
acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att	1572
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile	
370 375 380	
gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat	1620
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His	
385 390 395 400	
gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac	1668
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp	
405 410 415	
agc tgc gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc	1716
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro	
420 425 430	
ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca	1764
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr	
435 440 445	
tgg cat gac att acc gga aac cgt tgc gag ccg gtt gtc atc aat tgc	1812
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser	
450 455 460	

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat 1860
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480

gtt caa aga tag aagagcagag aggacggatt tcctgaagga aatccgtttt 1912
 Val Gln Arg

tttatattt 1920

<210> 8
 <211> 483
 <212> PRT
 <213> Bacillus licheniformis

<400> 8

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15

Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
 20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
 85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
 100 105 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
 115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
 130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
290 295 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480

Val Gln Arg

<210> 9
 <211> 2084
 <212> DNA
 <213> Bacillus amyloliquefaciens

<220>
 <221> CDS
 <222> (343)..(1794)
 <223> BAN

<400> 9
 gccccgcaca tacgaaaaga ctggctgaaa acattgagcc tttgatgact gatgatttgg 60
 ctgaagaagt ggatcgattg tttgagaaaa gaagaagacc ataaaaatac cttgtctgtc 120
 atcagacagg gtatttttta tgctgtccag actgtccgct gtgtaaaaat aaggaataaa 180
 ggggggttgt tattatttta ctgatatgta aaatataatt tgtataagaa atgagaggg 240
 agaggaaaca tgattcaaaa acgaaagcgg acagtttcgt tcagacttgt gcttatgtgc 300
 acgctgttat ttgtcagttt gccgattaca aaaacatcag cc gta aat ggc acg 354
 Val Asn Gly Thr
 1
 ctg atg cag tat ttt gaa tgg tat acg ccg aac gac ggc cag cat tgg 402
 Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp Gly Gln His Trp
 5 10 15 20
 aaa cga ttg cag aat gat gcg gaa cat tta tcg gat atc gga atc act 450
 Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp Ile Gly Ile Thr
 25 30 35
 gcc gtc tgg att cct ccc gca tac aaa gga ttg agc caa tcc gat aac 498
 Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln Ser Asp Asn
 40 45 50
 gga tac gga cct tat gat ttg tat gat tta gga gaa ttc cag caa aaa 546
 Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Gln Gln Lys
 55 60 65

ggg acg gtc aga acg aaa tac ggc aca aaa tca gag ctt caa gat gcg Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu Gln Asp Ala 70 75 80	594
atc ggc tca ctg cat tcc cgg aac gtc caa gta tac gga gat gtg gtt Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly Asp Val Val 85 90 95 100	642
ttg aat cat aag gct ggt gct gat gca aca gaa gat gta act gcc gtc Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp Val Thr Ala Val 105 110 115	690
gaa gtc aat ccg gcc aat aga aat cag gaa act tcg gag gaa tat caa Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser Glu Glu Tyr Gln 120 125 130	738
atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt gga aac acg tac Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg Gly Asn Thr Tyr 135 140 145	786
agt gat ttt aaa tgg cat tgg tat cat ttc gac gga gcg gac tgg gat Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Ala Asp Trp Asp 150 155 160	834
gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt ggg gaa gga aaa Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg Gly Glu Gly Lys 165 170 175 180	882
gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac tat gac tat tta Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr Asp Tyr Leu 185 190 195	930
atg tat gct gat gtt gac tac gac cac cct gat gtc gtg gca gag aca Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val Val Ala Glu Thr 200 205 210	978
aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca tta gac gcc ttc Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser Leu Asp Gly Phe 215 220 225	1026
cgt att gat gcc gcc aaa cat att aaa ttt tca ttt ctg cgt gat tgg Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe Leu Arg Asp Trp 230 235 240	1074
gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg ttt acg gtt gcg Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met Phe Thr Val Ala 245 250 255 260	1122
gag tat tgg cag aat aat gcc ggg aaa ctc gaa aac tac ttg aat aaa Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn Tyr Leu Asn Lys 265 270 275	1170
aca agc ttt aat caa tcc gtg ttt gat gtt ccg ctt cat ttc aat tta Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu His Phe Asn Leu 280 285 290	1218
cag gcg gct tcc tca caa gga ggc gga tat gat atg agg cgt ttg ctg Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met Arg Arg Leu Leu 295 300 305	1266

gac ggt acc gtt gtg tcc agg cat ccg gaa aag gcg gtt aca ttt gtt Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala Val Thr Phe Val 310 315 320	1314
gaa aat cat gac aca cag ccg gga cag tca ttg gaa tcg aca gtc caa Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val Gln 325 330 335 340	1362
act tgg ttt aaa ccg ctt gca tac gcc ttt att ttg aca aga gaa tcc Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu Ser 345 350 355	1410
ggt tat cct cag gtg ttc tat ggg gat atg tac ggg aca aaa ggg aca Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly Thr 360 365 370	1458
tcg cca aag gaa att ccc tca ctg aaa gat aat ata gag ccg att tta Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile Glu Pro Ile Leu 375 380 385	1506
aaa gcg cgt aag gag tac gca tac ggg ccc cag cac gat tat att gac Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His Asp Tyr Ile Asp 390 395 400	1554
cac ccg gat gtg atc gga tgg acg agg gaa ggt gac agc tcc gcc gcc His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ser Ser Ala Ala 405 410 415 420	1602
aaa tca ggt ttg gcc gct tta atc acg gac gga ccc ggc gga tca aag Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ser Lys 425 430 435	1650
cgg atg tat gcc ggc ctg aaa aat gcc ggc gag aca tgg tat gac ata Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr Trp Tyr Asp Ile 440 445 450	1698
acg ggc aac cgt tca gat act gta aaa atc gga tct gac ggc tgg gga Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser Asp Gly Trp Gly 455 460 465	1746
gag ttt cat gta aac gat ggg tcc gtc tcc att tat gtt cag aaa taa Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr Val Gln Lys 470 475 480	1794

ggtaataaaaa aaacacctcc aagctgagtg cgggtatcag cttggaggtg cgtttatattt	1854
ttcagccgta tgacaaggtc ggcatcaggt gtgacaaata cggatatgctg gctgtcatag	1914
gtgacaaatc cgggtttttgc gccgtttggc tttttcacat gtctgatttt tgtataatca	1974
acaggcacgg agccggaatc tttcgcttg gaaaaataag cggcgatcgt agctgcttcc	2034
aatatggatt gttcatcggg atcgctgctt ttaatcacia cgtgggatcc	2084

<210> 10
 <211> 483
 <212> PRT
 <213> Bacillus amyloliquefaciens
 <400> 10

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
1 5 10 15

Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
20 25 30

Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
35 40 45

Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60

Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65 70 75 80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
85 90 95

Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
100 105 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
115 120 125

Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
130 135 140

Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145 150 155 160

Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
165 170 175

Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
195 200 205

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
210 215 220

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225 230 235 240

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
260 265 270

Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
275 280 285

His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
290 295 300

Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305 310 315 320

Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385 390 395 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
435 440 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
450 455 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Lys

<210> 11
 <211> 1458
 <212> DNA
 <213> Bacillus sp.

<220>
 <221> CDS
 <222> (1)..(1458)
 <223> AA560

<400> 11
 cac cat aat ggt acg aac ggc aca atg atg cag tac ttt gaa tgg tat 48
 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
 1 5 10 15
 cta cca aat gac gga aac cat tgg aat aga tta agg tct gat gca agt 96
 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
 20 25 30
 aac cta aaa gat aaa ggg atc tca gcg gtt tgg att cct cct gca tgg 144
 Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
 35 40 45
 aag ggt gcc tct caa aat gat gtg ggg tat ggt gct tat gat ctg tat 192
 Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60
 gat tta gga gaa ttc aat caa aaa gga acc att cgt aca aaa tat gga 240
 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly
 65 70 75 80
 acg cgc aat cag tta caa gct gca gtt aac gcc ttg aaa agt aat gga 288
 Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly
 85 90 95
 att caa gtg tat ggc gat gtt gta atg aat cat aaa ggg gga gca gac 336
 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110
 gct acc gaa atg gtt agg gca gtt gaa gta aac ccg aat aat aga aat 384
 Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
 115 120 125
 caa gaa gtg tcc ggt gaa tat aca att gag gct tgg aca aag ttt gac 432
 Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
 130 135 140
 ttt cca gga cga ggt aat act cat tca aac ttc aaa tgg aga tgg tat 480
 Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
 145 150 155 160
 cac ttt gat gga gta gat tgg gat cag tca cgt aag ctg aac aat cga 528
 His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg
 165 170 175
 att tat aaa ttt aga ggt gat gga aaa ggg tgg gat tgg gaa gtc gat 576
 Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp

180	185	190	
aca gaa aac ggt aac tat gat tac cta atg tat gca gat att gac atg Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met 195 200 205			624
gat cac cca gag gta gtg aat gag cta aga aat tgg ggt gtt tgg tat Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr 210 215 220			672
acg aat aca tta ggc ctt gat ggt ttt aga ata gat gca gta aaa cat Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His 225 230 235 240			720
ata aaa tac agc ttt act cgt gat tgg att aat cat gtt aga agt gca Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala 245 250 255			768
act ggc aaa aat atg ttt gcg gtt gcg gaa ttt tgg aaa aat gat tta Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu 260 265 270			816
ggt gct att gaa aac tat tta aac aaa aca aac tgg aac cat tca gtc Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val 275 280 285			864
ttt gat gtt ccg ctg cac tat aac ctc tat aat gct tca aaa agc gga Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly 290 295 300			912
ggg aat tat gat atg agg caa ata ttt aat ggt aca gtc gtg caa aga Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg 305 310 315 320			960
cat cca atg cat gct gtt aca ttt gtt gat aat cat gat tcg caa cct His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro 325 330 335			1008
gaa gaa gct tta gag tct ttt gtt gaa gaa tgg ttc aaa cca tta gcg Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala 340 345 350			1056
tat gct ttg aca tta aca cgt gaa caa ggc tac cct tct gta ttt tat Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr 355 360 365			1104
gga gat tat tat ggc att cca acg cat ggt gta cca gcg atg aaa tcg Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser 370 375 380			1152
aaa att gac ccg att cta gaa gcg cgt caa aag tat gca tat gga aga Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg 385 390 395 400			1200
caa aat gac tac tta gac cat cat aat atc atc ggt tgg aca cgt gaa Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu 405 410 415			1248
ggg aat aca gca cac ccc aac tcc ggt tta gct act atc atg tcc gat Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp 420 425 430			1296

ggg gca gga gga aat aag tgg atg ttt gtt ggg cgt aat aaa gct ggt 1344
 Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
 435 440 445

caa gtt tgg acc gat atc act gga aat cgt gca ggt act gtt acg att 1392
 Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile
 450 455 460

aat gct gat gga tgg ggt aat ttt tct gta aat gga gga tca gtt tct 1440
 Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
 465 470 475 480

att tgg gta aac aaa taa 1458
 Ile Trp Val Asn Lys
 485

<210> 12
 <211> 485
 <212> PRT
 <213> Bacillus sp.

<400> 12

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
 20 25 30

Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
 35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly
 65 70 75 80

Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly
 85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
 115 120 125

Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
 130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
290 295 300

Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg

385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Asn Lys
485

<210> 13
<211> 485
<212> PRT
<213> bacillus sp. 707

<400> 13

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly His Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Gln Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
290 295 300

Gly Asn Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg
305 310 315 320

His Pro Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys
385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Asn Lys
485

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<211> 60
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<213> Artificial Sequence

<220>
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<210> 15
<211> 21
<212> DNA
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<220>
<223> Primer

<400> 15
gaatttgtag atacgatttt g 21

<210> 16

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
cgattgctga cgctgttatt tgcg

24

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
cttggtccct tgtcagaacc aatg

24

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
gtcatagttg ccgaaatctg tatcgacttc

30

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
gacctgcagt caggcaacta

20

<210> 20
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
tagagtcgac ctgcaggcat

20